

ATTACHMENT A

Amino Acid Sequences of the Variable Domains of Bevacizumab

Variable Heavy

A.4.6.1	<u>EIQLVQSGPEIKQPGETVRISCKASGYTETNYGMNWVKQAPGKGLKWMG</u>
	* * * * * * * * *
F(ab)-12	<u>EVQLVESGGGLVQPGGSLRLSCAASGYTETNYGMNWVRQAPGKGLEWVG</u>
	* * * * *
humIII	EVQLVESGGGLVQPGGSLRLSCAASGFTESSYAMSNVROAPGKCLEWVS
	1 10 20 30 40
A.4.6.1	<u>WINTYTGEPTYAADEKRRTFSLETSASTAYLQISNLKNDDTATYFCAK</u>
	* * * * * * * * *
F(ab)-12	<u>WINTYTGEPTYAADEKRRTFSLDTSKSTAYLQMSLRAEDTAVYYCAK</u>
	* * * * * * * * *
humIII	VISGDDGGSTYYADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCAR
	50 a 60 70 80 abc 90
A.4.6.1	<u>XPHYYGSSHWYFDYWGAGITVTVSS</u>
	* *
F(ab)-12	<u>XPHYYGSSHWYFDYWGQGTLTVSS</u>
	*
humIII	G-----FDYWGQGT L TVSS
	110

Variable Light

A.4.6.1	DIQMTQTSSLSASLGDRVII <u>SCASODISNYLNWYQQKPDTVKVL</u> IY
	* * * * *
F(ab)-12	DIQMTQSPSSLSASVGDRVIT <u>CSASODISNYLNWYQQKP</u> GA <u>PKV</u> LIY
	* * * * *
humKI	DIQMTQSPSSLSASVGDRVITCRASQSISNYLA <u>WYQQKP</u> GA <u>PKL</u> LIY
	1 10 20 30 40
A.4.6.1	<u>FTSSLHSGVP</u> SRFSGSGSGTDYSLTISNLEPEDIATYYCQQYSTVFWTF
	** * * *
F(ab)-12	<u>FTSSLHSGVP</u> SRFSGSGSGTDFTLT <u>ISSLQ</u> PEDFATYYCQQYSTVFWTF

humKI	AASSLES <u>GVPSRFSGSGSGTDFTL</u> T <u>ISSLQ</u> PEDFATYYCQQYN <u>SLPWT</u> F
	50 60 70 80 90
A.4.6.1	GGGTKLEIKR
	* *
F(ab)-12	<u>GQG</u> TKVEIKR
humKI	<u>GQG</u> TKVEIKR
	100

Fig. 1. Amino acid sequence of variable heavy and light domains of muMAbVEGF A.4.6.1, humanized F(ab) with optimal VEGF binding [F(ab)-12] and human consensus frameworks (*humIII*, heavy subgroup III; *humKI*, light κ subgroup I). Asterisks, differences between humanized F(ab)-12 and the murine MAb or between F(ab)-12 and the human framework. CDRs are *underlined*.